

AMENDMENTS TO THE CLAIMS

Listing of claims:

1. (Currently amended) ~~The use of~~ A method for identifying herbicides comprising utilizing a nuclear encoded Clp-protease in a method for identifying herbicides.
2. (Currently amended) The ~~use~~ method as claimed in claim 1, wherein the Clp-protease is
 - a) selected from the group consisting of ClpP1-protease, ClpP2-protease, ClpP3-protease, ClpP4-protease and ClpP6-protease; or
 - b) selected from the group consisting of ClpR1-protease, ClpR3-protease, and ClpR4-protease; or
 - c) ClpP-like-protease.
3. (Currently amended) ~~A~~ An isolated plant nucleic acid sequence encoding a ClpP2-protease comprising:
 - a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:3, or
 - b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:4 by backtranslating, or
 - c) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:3 which has an identity with SEQ ID NO:3 of ~~has~~ at least 66%.
4. (Currently amended) ~~A~~ An isolated plant nucleic acid sequence encoding a ClpR1-protease comprising:
 - a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:11, or
 - b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:12 by backtranslating, or

- c) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:11 which has an identity with SEQ ID NO:11 of ~~has~~ at least 69%.
5. (Currently amended) A plant nucleic acid sequence encoding a ClpP-like-protease comprising:
- a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:17, or
 - b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:18 by backtranslating, or
 - c) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:17 which has an identity with SEQ ID NO:17 of ~~has~~ at least 67%.
6. (Currently amended) A polypeptide with the activity of a nuclear encoded Clp-protease, encoded by a nucleic acid molecule as claimed in claim 3, ~~4 or 5~~.
7. (Currently amended) An expression cassette comprising
- a) ~~genetic control sequences in operable linkage with a nucleic acid sequence as claimed in claim 3, 4 or 5; or~~
 - b) ~~and optionally one or more additional functional elements, or~~
 - e) ~~a combination of a) and b).~~
8. (Original) A vector comprising an expression cassette as claimed in claim 7.
9. (Currently amended) A transgenic organism comprising at least one nucleic acid sequence as claimed in claim 4, ~~5 or 6 encoding a polypeptide with the activity of a Clp-protease, an expression cassette as claimed in claim 7 or a vector as claimed in claim 8~~, selected from among the group consisting of bacteria, yeasts, fungi, animal cells or plant cells animals, and plants.

10. (Currently amended) A method for identifying substances with herbicidal activity, comprising the following steps:

- i. bringing a nuclear encoded Clp-protease into contact with one or more test compounds under conditions which permit the test compound(s) to bind to ~~the~~ a nucleic acid molecule encoding a Clp-protease or to the nuclear encoded Clp-protease, and
- ii. detecting whether the test compound binds to the Clp-protease ~~of i~~), or
- iii. detecting whether the test compound reduces or blocks the enzymatic or biological activity of the Clp-protease ~~of i~~), or
- iv. detecting whether the test compound reduces or blocks the transcription, translation or expression of the Clp-protease ~~of i~~).

11. (Currently amended) A The method as claimed in claim 10, wherein the Clp-protease is

- a) selected from the group consisting of ClpP1-protease, ClpP2-protease, ClpP3-protease, ClpP4-protease and ClpP6-protease; or
- b) selected from the group consisting of ClpR1-protease, ClpR3-protease, and ClpR4-protease; or
- c) ClpP-like-protease.

12. (Currently amended) A The method as claimed in claim 10, wherein

- a) the ClpP1-protease is encoded by a nucleic acid sequence which comprises:
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1, or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:2 by back translating, or

- iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:1 which has an identity with SEQ ID NO:1 of ~~has~~ at least 50%;
- b) the ClpP2-protease is encoded by a nucleic acid sequence which comprises:
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:3, or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:4 by back translating, or
 - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:3 which has an identity with SEQ ID NO:3 of ~~has~~ at least 50%;
- c) the ClpP3-protease is encoded by a nucleic acid sequence which comprises:
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:5, or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:6 by back translating, or
 - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:5 which has an identity with SEQ ID NO:5 of ~~has~~ at least 50%;
- d) the ClpP4-protease is encoded by a nucleic acid sequence which comprises:
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:7, or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:8 by back translating, or

- iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:7 which has an identity with SEQ ID NO:7 of ~~has~~ at least 50%;
- e) the ClpP6-protease is encoded by a nucleic acid sequence which comprises:
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:9,
or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:10 by back translating, or
 - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:9 which has an identity with SEQ ID NO:9 of ~~has~~ at least 50%;
- f) the ClpR1-protease is encoded by a nucleic acid sequence which comprises:
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:11,
or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:12 by back translating, or
 - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:11 which has an identity with SEQ ID NO:11 of ~~has~~ at least 50%;
- g) the ClpR3-protease is encoded by a nucleic acid sequence which comprises:
- i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:13,
or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:14 by back translating, or

- iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:13 which has an identity with SEQ ID NO:13 of ~~has~~ at least 50%;
 - h) the ClpR4-protease is encoded by a nucleic acid sequence which comprises:
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:15, or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:16 by back translating, or
 - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:15 which has an identity with SEQ ID NO:15 of ~~has~~ at least 50%;
 - i) the ClpP like-protease is encoded by a nucleic acid sequence which comprises:
 - i) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:17, or
 - ii) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:18 by back translating, or
 - iii) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:17 which has an identity with SEQ ID NO:17 of ~~has~~ at least 50%;
13. (Currently amended) A The method as claimed in claim 10 [~~11 or 12~~], wherein a test compound is selected which reduces or blocks the enzymatic or biological activity of Clp-protease.
14. (Currently amended) A The method as claimed in ~~any of claims 10, 11, 12 or 13~~ claim 10, wherein

- i. either Clp-protease is expressed in a transgenic organism or an organism which naturally contains Clp-protease is grown,
- ii. the Clp-protease of step i) is brought into contact with a test compound in the cell digest of the transgenic or nontransgenic organism, in partially purified form or in homogeneously purified form, and
- iii. selecting a test compound which reduces or blocks the enzymatic activity of the Clp-protease of step a).

15. (Currently amended) A The method as claimed in ~~any of claims 10, 11, 12 or 13~~ claim 10, which comprises the following steps:

- i. generating a transgenic organism comprising a nucleic acid sequence encoding Clp-protease, wherein Clp-protease is expressed recombinantly;
- ii. applying a test substance to the transgenic organism of i) and to a nontransgenic organism of the same genotype,
- iii. determining the growth or the viability of the transgenic plant and the nontransgenic plant after application of the test ~~compound~~ substance, and
- iv. selecting a test substance[[s]] which bring about a reduced growth of the nontransgenic plant in comparison with the growth of the transgenic plant.

16. (Currently amended) A The method as claimed in claim 15, which is carried out in a plant organism, a cyanobacterium or proteobacterium.

17. (Currently amended) A method for identifying substances with growth-regulatory activity, which comprises the following steps:

- i. generating a transgenic plant comprising a nucleic acid sequence Clp-protease, wherein Clp-protease is expressed recombinantly;

- ii. applying a test substance to the transgenic plant of i) and to a nontransgenic plant of the same variety,
 - iii. determining the growth or the viability of the transgenic plant and the nontransgenic plant after application of the test ~~compound~~ substance, and
 - iv. selecting a test substance[[s]] which bring about a reduced growth of the nontransgenic plant in comparison with the growth of the transgenic plant.
18. (Currently amended) A The method as claimed in any of claims 10 to 17 claim 10, wherein the substances are identified ~~in~~ by a high-throughput screening method.
19. (Currently amended) A support comprising one or more of the nucleic acid molecules as claimed in claim 3, ~~4, or 5~~ one or more expression cassettes as claimed in claim 7, one or more vectors as claimed in claim 8, one or more organisms as claimed in claim 9 or one or more (poly)peptides as claimed in claim 6.
20. (Currently amended) A The method as claimed in any of claims 10 to 18 claim 10, wherein the substances are identified ~~in~~ by High-Throughput Screening using a support as ~~claimed in claim 19~~ comprising one or more nucleic acid molecules comprising a plant nucleic acid sequence encoding a ClpP2-protease comprising:
- a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:3, or
 - b) a nucleic acid sequence which, owing to the degeneracy of the genetic code, can be deduced from the amino acid sequence shown in SEQ ID NO:4 by backtranslating, or
 - c) a functional equivalent of nucleic acid sequence shown in SEQ ID NO:3 which has an identity with SEQ ID NO:3 of at least 66%.
21. (Currently amended) ~~The use of~~ A method for controlling undesired vegetation and/or for regulating the growth of plants which comprises utilizing a compound with herbicidal activity, identified by one of the method[[s]] as claimed in any of claims 10 to 16, 18 and 20 claim 10 for controlling undesired vegetation and/or for regulating the growth of plants.

22. (Currently amended) ~~The use of~~ A method for controlling undesired vegetation and/or for regulating the growth of plants which comprises utilizing a compound with growth-regulatory activity, identified by the method as claimed in claim 17 ~~any of claims 17, 18 or 20 for controlling undesired vegetation and/or for regulating the growth of plants.~~

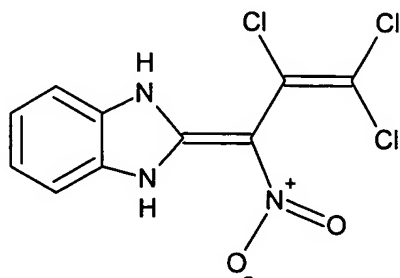
23. (Currently amended) A method for the preparation of an agrochemical composition, which comprises

- a) identifying a compound with herbicidal activity by ~~one of the method~~[[s]] as claimed in ~~any of claims 10 to 16, 18 and 20~~ claim 10 ~~or a compound with growth-regulatory activity as claimed in any of claims 17, 18 or 20, and~~
- b) formulating this compound together with suitable auxiliaries to give crop protection products with herbicidal or growth-regulatory activity.

24. (Currently amended) ~~The use of~~ A method for controlling undesired vegetation and/or for regulating the growth of plants comprising utilizing at least one Clp-protease inhibitor identified by ~~one of the method~~[[s]] as claimed in ~~any of claims 10 to 16, 18 and 20~~ claim 10 ~~in a method for controlling undesired vegetation and/or for regulating the growth of plants.~~

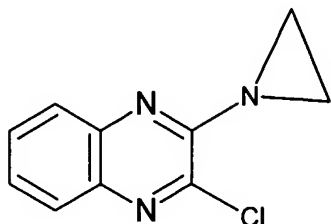
25. (Currently amended) A method for controlling undesired vegetation and/or for regulating the growth of plants comprising treating said ~~weeds~~ undesired vegetation or plants with a herbicide, wherein said herbicide is a compound which is a inhibitor of a Clp-protease.

26. (Currently amended) A Clp-protease inhibitor of the formula:



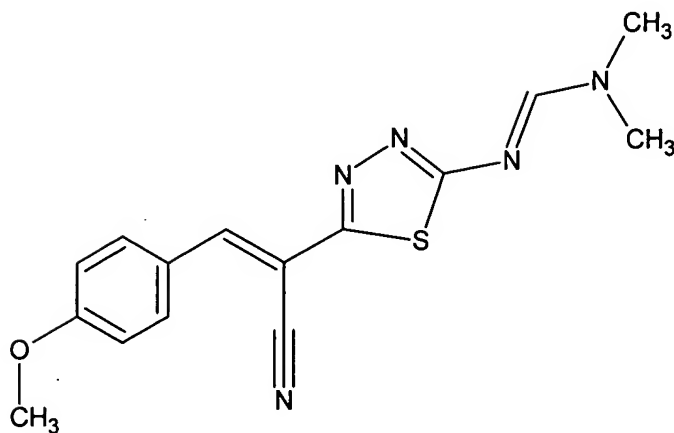
formula (I)

or



formula (II)

or



formula (III).

27. (New) A polypeptide with the activity of a nuclear encoded Clp-protease, encoded by a nucleic acid molecule as claimed in claim 4.
29. (New) A transgenic organism comprising an expression cassette as claimed in claim 7, selected from the group consisting of bacteria, yeasts, fungi, animals, and plants.
30. (New) A transgenic organism comprising a vector as claimed in claim 8, selected from the group consisting of bacteria, yeasts, fungi, animals, and plants.
31. (New) The method as claimed in claim 17, wherein the substances are identified by high-throughput screening.
32. (New) A support comprising one or more expression cassettes as claimed in claim 7.

33. (New) A method for the preparation of an agrochemical composition, which comprises
- a) identifying a compound with growth-regulatory activity as claimed in claim 17, and
 - b) formulating this compound together with suitable auxiliaries to give crop protection products with herbicidal or growth-regulatory activity.
34. (New) An expression cassette comprising genetic control sequences in operable linkage with a nucleic acid sequence as claimed in claim 4 and optionally one or more additional functional elements.
35. (New) An expression cassette comprising genetic control sequences in operable linkage with a nucleic acid sequence as claimed in claim 5 and optionally one or more additional functional elements.
36. (New) The expression cassette of claim 7, wherein the additional functional elements are selected from the group consisting of reporter genes, replication origins, selection markers, affinity tags, and sequences which target products into apoplasts, plastids, vacuoles, mitochondria, peroxisomes, endoplasmatic reticulum (ER), or cytosol.